

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence selected from the group consisting of:

(a) a polynucleotide fragment of SEQ ID NO:1 or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No: PTA-4803, which is hybridizable to SEQ ID NO:1;

(b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:2 or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No: PTA-4803, which is hybridizable to SEQ ID NO:1;

(c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:2 or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No: PTA-4803, which is hybridizable to SEQ ID NO:1;

(d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:2 or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No: PTA-4803, which is hybridizable to SEQ ID NO:1;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:2 or the cDNA sequence included in ATCC Deposit No: PTA-4803, which is hybridizable to SEQ ID NO:1, having phosphatase activity;

(f) a polynucleotide which is a variant of SEQ ID NO:1;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:1;

(h) an isolated polynucleotide comprising nucleotides 29 to 763 of SEQ ID NO:1, wherein said nucleotides encode a polypeptide corresponding to amino acids 2 to 246 of SEQ ID NO:2 minus the start methionine;

(i) an isolated polynucleotide comprising nucleotides 26 to 763 of SEQ ID NO:1, wherein said nucleotides encode a polypeptide corresponding to amino acids 2 to 246 of SEQ ID NO:2 including the start codon;

(j) a polynucleotide which represents the complimentary sequence (antisense) of SEQ ID NO:1; and

(k) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment consists of a nucleotide sequence encoding a human phosphatase.
3. A recombinant vector comprising the isolated nucleic acid molecule of
5 claim 1.
4. A recombinant host cell comprising the vector sequences of claim 3.
5. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:
 - (a) a polypeptide fragment of SEQ ID NO:2 or the encoded sequence
10 included in ATCC Deposit No: PTA-4803;
 - (b) a polypeptide fragment of SEQ ID NO:2 or the encoded sequence included in ATCC Deposit No: PTA-4803, having phosphatase activity;
 - (c) a polypeptide domain of SEQ ID NO:2 or the encoded sequence included in ATCC Deposit No: PTA-4803;
 - 15 (d) a polypeptide epitope of SEQ ID NO:2 or the encoded sequence included in ATCC Deposit No: PTA-4803;
 - (e) a full length protein of SEQ ID NO:2 or the encoded sequence included in ATCC Deposit No: PTA-4803;
 - (f) a polypeptide comprising amino acids 2 to 246 of SEQ ID NO:2,
20 wherein said amino acids 2 to 246 comprising a polypeptide of SEQ ID NO:2 minus the start methionine; and
 - (g) a polypeptide comprising amino acids 1 to 246 of SEQ ID NO:2.
6. The isolated polypeptide of claim 5, wherein the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-
25 terminus.
7. An isolated antibody that binds specifically to the isolated polypeptide of claim 5.
8. A recombinant host cell that expresses the isolated polypeptide of claim
5.
- 30 9. A method of making an isolated polypeptide comprising:
 - (a) culturing the recombinant host cell of claim 8 under conditions such that said polypeptide is expressed; and

(b) recovering said polypeptide.

10. The polypeptide produced by claim 9.

11. A method for preventing, treating, or ameliorating a medical condition, comprising the step of administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 5, or a modulator thereof.

12. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and

10 (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

13. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

15 (a) determining the presence or amount of expression of the polypeptide of claim 5 in a biological sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

14. An isolated nucleic acid molecule consisting of a polynucleotide having a nucleotide sequence selected from the group consisting of:

20 (a) a polynucleotide encoding a polypeptide of SEQ ID NO:2;

(b) an isolated polynucleotide consisting of nucleotides 29 to 763 of SEQ ID NO:1, wherein said nucleotides encode a polypeptide corresponding to amino acids 2 to 246 of SEQ ID NO:2 minus the start codon;

25 (c) an isolated polynucleotide consisting of nucleotides 26 to 763 of SEQ ID NO:1, wherein said nucleotides encode a polypeptide corresponding to amino acids 1 to 246 of SEQ ID NO:2 including the start codon;

(d) a polynucleotide encoding the BMY_HPP13 polypeptide encoded by the cDNA clone contained in ATCC Deposit No. PTA-4803; and

30 (e) a polynucleotide which represents the complimentary sequence (antisense) of SEQ ID NO:1.

15. The isolated nucleic acid molecule of claim 14, wherein the polynucleotide comprises a nucleotide sequence encoding a human phosphatase.

16. A recombinant vector comprising the isolated nucleic acid molecule of claim 15.
17. A recombinant host cell comprising the recombinant vector of claim 16.
18. An isolated polypeptide consisting of an amino acid sequence selected from the group consisting of:
- (a) a polypeptide fragment of SEQ ID NO:2 having phosphatase activity;
 - (b) a polypeptide domain of SEQ ID NO:2 having phosphatase activity;
 - (c) a full length protein of SEQ ID NO:2;
 - (d) a polypeptide corresponding to amino acids 2 to 246 of SEQ ID NO:2, wherein said amino acids 2 to 246 consisting of a polypeptide of SEQ ID NO:2 minus the start methionine;
 - (e) a polypeptide corresponding to amino acids 1 to 246 of SEQ ID NO:2;
 - (f) a polypeptide encoded by the cDNA contained in ATCC Deposit No. PTA-4803.
19. The method of diagnosing a pathological condition of claim 12 wherein the condition is a member of the group consisting of: a disorder related to aberrant phosphatase-dependent signaling; a disorder related to aberrant phosphatase-dependent cell cycle regulation; a disorder related to aberrant dual-specificity phosphatase activity, a metabolic disorder, diabetes, cardiovascular disorders, immune disorders, gastrointestinal disorders, and female reproductive disorders.
20. The method for preventing, treating, or ameliorating a medical condition of claim 11, wherein the medical condition is selected from the group consisting of: aberrant phosphatase-dependent signaling; a disorder related to aberrant phosphatase-dependent cell cycle regulation; a disorder related to aberrant dual-specificity phosphatase activity, a metabolic disorder, diabetes, cardiovascular disorders, immune disorders, gastrointestinal disorders, and female reproductive disorders.
21. A method of isolating phosphoproteins or phosphopeptides comprising the steps of passing a sample over a catalytically inactive mutant of the polypeptide provided in SEQ ID NO:2 bound to a support, washing sample material away that did not bind to said polypeptide, and isolating said bound sample by subjecting said bound sample / polypeptide complex under conditions in which said bound sample is released.

22. A computer for producing a three-dimensional representation of a molecule or molecular complex, wherein said molecule or molecular complex comprises the structural coordinates of the BMY_HPP13 model provided in Figure 8 in accordance with Table IV wherein said computer comprises:

- 5 (a) A machine-readable data storage medium, comprising a data storage material encoded with machine readable data, wherein the data is defined by the set of structure coordinates of the model;
- (b) a working memory for storing instructions for processing said machine-readable data;
- 10 (c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium for processing said machine readable data into said three-dimensional representation; and
- (d) a display coupled to said central-processing unit for displaying said three-dimensional representation.

15 23. A method for identifying a mutant with altered biological properties, function, or activity of BMY_HPP13 wherein said method comprises the steps of:

- (a) using a model of said polypeptide according to the structural coordinates of said model to identify amino acids to mutate; and
- (b) mutating said amino acids to create a mutant protein with altered
- 20 biological function or properties.

24. A method for designing or selecting compounds as potential modulators of BMY_HPP13 wherein said method comprises the steps of:

- (a) identifying a structural or chemical feature of said member using the structural coordinates of said member; and
- 25 (b) rationally designing compounds that bind to said feature.